IN THE SPECIFICATION:

Please replace the first full paragraph on page 9 with the following.

When using single conserved bases as the inner alignment points, it is desirable to avoid selection of inner alignment points from regions of sequence where the electrophoretic resolution R is low (R~1). This is because, in a region of low resolution, it will be very hard to detect the proper alignment points within a homopolymeric subsequence of bases. For example, consider positions 417-429 of the HIV-1 fragment produced in Example 1 below. The wild-type sequence is 5'-GAAAAAATAAAG-3' (SEQ ID NO: 1), and with >98% certainty, based on an alignment of HIV-1 sequences of different subtypes, positions 418, 420, 421, and 423 are expected to be "A". However, if the electrophoretic resolution happens to be low in this region, then it may be difficult to distinguish all the individual "A" residues within this subsequence.

Please replace Table 5 on page 21 with the following.

Table 5. Reference Multiplets for Strategy Which Involves Cross-Lane Alignments.

Position	Length	Sequence	Probability ratio*
402-424	23	TGG CCN TTN ACA GAA GAA AAN AT (SEQ ID NO: 2)	4^{40} ☐ 10^{12}
450-457	8	GAN ATG GA (SEQ ID NO: 3)	4^{7} ☐ 16,000
462-472	11	GAN GGN AAN AT (SEQ ID NO: 4)	4^{8} ☐ 65,000
480-499	20	ATN GGG CCT GAA AAT CCA TA (SEQ ID NO: 5)	4^{19} ☐ $3 \cdot 10^{11}$

*ratio of probabilities of finding the specified sequence, based on either (1) an alignment of N=146 sequences of all major HIV-1 subtypes as described in Table 2, or (2) a completely random occurrence, computed by means of Kolmogorov probability model (see Feller, W. (1968) An Introduction to Probability Theory and its Applications. Volume I, 3rd Edition. J. Wiley & Sons, New York.).